



Government of India
Ministry of Science & Technology
Department of Biotechnology
सत्यमेव जयते



ONE DAY ONE GENOME

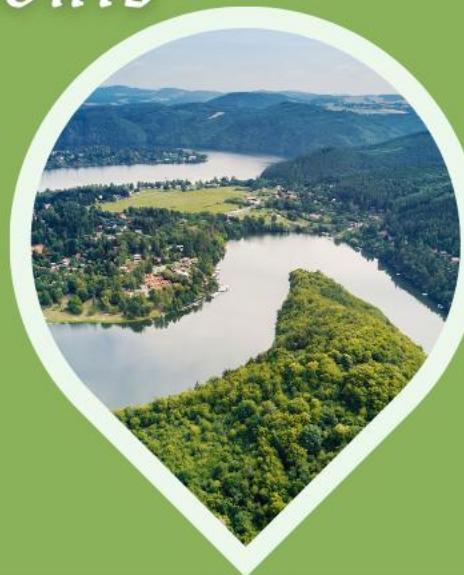
Acinetobacter kanungonis



Degradation pathway genes



Ecological versatility



Isolated from the skin of
freshwater pufferfish collected
from the Mahanadi River in India

Acinetobacter kanungonis sp. nov. (PS-1^T)

Genome Accession Number: JAACKC000000000

Quality of Genome Assembly and Annotation:

Results from indigenously developed **BHARAT** analysis pipeline: (**Bacterial Hybrid genome Assembly and Rapid Annotation Toolset**)

Table 1: Assembly Details

Contigs	34
GC Content	41.97
Contig L50	5
Genome length	3,506,843 bp
Contig N50	265,534

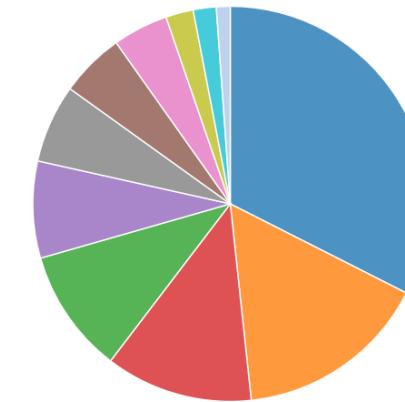
Table 2: Annotated Genome Features

CDS	3,344
tRNA	66
Repeat Regions	3
rRNA	0

Table 3: Antimicrobial Resistance Genes

AMR Mechanism	Genes
Antibiotic target in susceptible species	Alr, Ddl, dxr, EF-G, EF-Tu, folA, Dfr, folP, gyrA, gyrB, inhA, fabI, Iso-tRNA, MurA, rho, rpoB, rpoC, S10p, S12p
Efflux pump conferring antibiotic resistance	EmrAB-TolC, MacA, MacB, MdfA/Cmr, TolC/OpmH
Regulator modulating expression of antibiotic resistance genes	OxyR
Protein modulating permeability to antibiotic	OprB, OprD family
Protein altering cell wall charge conferring antibiotic resistance	GdpD, PgsA

Subsystem Analysis



Subsystem (Subsystems, Genes)

- METABOLISM (86, 593)
- PROTEIN PROCESSING (42, 222)
- STRESS RESPONSE, DEFENSE, VIRULENCE (32, 117)
- ENERGY (27, 209)
- MEMBRANE TRANSPORT (21, 102)
- DNA PROCESSING (17, 64)
- RNA PROCESSING (14, 75)
- CELLULAR PROCESSES (12, 73)
- CELL ENVELOPE (6, 39)
- MISCELLANEOUS (5, 17)
- REGULATION AND CELL SIGNALING (3, 12)

Genome Assembly

